

SEQUENCE LISTING

5 <110> Sera, Takashi
 <120> Zinc Finger Domain Recognition Code and Uses Thereof
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 10 <140> US 09/911,261
 <141> 2001-07-23
 <150> US 60/220,060
 <151> 2000-07-21
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 <170> PatentIn version 3.0
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 <223> Amino acids 1-3, 10-21 and 29-32 are Xaa wherein Xaa = any amino acid.
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 <223> Amino acids 5-8 are Xaa wherein Xaa = any amino acid, and up to two can be missing.
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    amino acid.

    <220>
15  <221>  VARIANT
    <222>  (5)..(8)
    <223>  Amino acids 5-8 are Xaa wherein Xaa = any amino acid, and up
    to two can be missing.

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    <223>  Amino acids 23-27 are Xaa wherein Xaa = any amino acid, and up
    to two can be missing.

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25  <221>  VARIANT
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    <223>  Amino acid 15 is Xaa wherein Xaa = Z-1 wherein Z-1 = Arg or Lys,
30  Gln or Asn, Thr, Met, Leu or Ile, or Glu or Asp.

    <220>
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    <222>  (17)..(17)
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    Asn, Gln, Thr, Val or Ala, or Asp or Glu.

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40  <222>  (18)..(18)
    <223>  Amino acid 18 is Xaa wherein Xaa = Z3 wherein Z3 = His or Lys,
    Asn or Gln, Ser, Ala or Met, or Asp or Glu.

    <220>
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    <222>  (21)..(21)
    <223>  Amino acid 21 is Xaa wherein Xaa = Z6 wherein Z6 = Arg or Lys,
    Gln or Asn, Thr, Tyr, Leu, Ile or Met, or Glu or Asp.

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55

Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa
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 Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
 35 40 45
 20 Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
 50 55 60
 Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
 65 70 75 80
 25 Arg Ser Asp Glu Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
 85 90 95
 30 Asp Gly Gly Gly Ser Gly Lys Lys Lys Gln His Ile Cys His Ile Gln
 100 105 110
 Gly Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu
 115 120 125
 35 Arg Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys
 130 135 140
 Gly Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr
 145 150 155 160
 His Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe
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 45 Met Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys
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 Lys Gly Gly Ser
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35 40 45
15 Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
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40 Met Glu Lys Leu Arg Asn Gly Ser Gly Asp Pro Gly Lys Lys Lys Gln
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45 Gln Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
35 40 45
Glu Cys Gly Lys Ser Phe Ser Arg Ser Ser His Leu Gln Gln His Gln
50 55 60
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 His Ala Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser Ser Asn Leu
 20 25 30
 Gln Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
 20 35 40 45
 Glu Cys Gly Lys Ser Phe Ser Glu Ser Ser Asp Leu Gln Arg His Gln
 50 55 60
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 Ser Phe Ser Arg Ser Asp His Leu Ser Arg His Gln Arg Thr His Gln
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 30 Asn Lys Lys

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 His Ala Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser Ser Asn Leu
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 50 Gln Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
 35 40 45
 Glu Cys Gly Lys Ser Phe Ser Arg Ser Ser His Leu Gln Glu His Gln
 50 55 60
 55 Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys

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	Gln	Arg	His	Gln	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Pro
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30	Glu	Cys	Gly	Lys	Ser	Phe	Ser	Gln	Ser	Ser	Asn	Leu	Gln	Arg	His	Gln
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	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Pro	Glu	Cys	Gly	Lys
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	Ser	Leu	Asp	Asp	Lys	Pro	Tyr	Lys	Cys	Thr	Glu	Cys	Glu	Lys	Ser	Phe	
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	Lys	Ser	His	Lys	Cys	Ala	Asp	Cys	Gly	Lys	Ser	Phe	Phe	Gln	Ser	Ser	
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	Asn	Leu	Ile	Gln	His	Arg	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	
				100					105					110			
20	Cys	Asp	Glu	Cys	Gly	Glu	Ser	Phe	Lys	Gln	Ser	Ser	Asn	Leu	Ile	Gln	
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	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Asp	Glu	Cys	
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	Gly	Arg	Cys	Phe	Ser	Gln	Ser	Ser	His	Leu	Ile	Gln	His	Gln	Arg	Thr	
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	His	Thr	Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Ser	Glu	Cys	Gly	Lys	Cys	Phe	
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	Ser	Gln	Ser	Ser	His	Leu	Arg	Gln	His	Met	Lys	Val	His	Lys	Glu	Glu	
				180					185					190			
35	Lys	Pro	Arg	Lys	Thr	Arg	Gly	Lys	Asn	Ile	Arg	Val	Lys	Thr	His	Leu	
			195					200					205				
	Pro	Ser	Trp	Lys	Ala	Gly	Thr	Glu	Gly	Ser	Leu	Trp	Leu	Val	Ser	Val	
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				20					25					30			

	Thr	Ala	Glu	Glu	Trp	Val	Ser	Tyr	Pro	Leu	Gln	Gln	Val	Thr	Asp	Leu	
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5	Leu	Val	His	Lys	Glu	Ala	His	Ala	Gly	Ile	Arg	Tyr	His	Ile	Cys	Ser	
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	Gln	Cys	Gly	Lys	Ala	Phe	Ser	Gln	Ile	Ser	Asp	Leu	Asn	Arg	His	Gln	
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	Gly	Phe	Ser	Arg	Ser	Ser	His	Leu	Ile	Gln	His	Gln	Arg	Thr	His	Thr	
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	Gly	Glu	Arg	Pro	Tyr	Asp	Cys	Asn	Glu	Cys	Gly	Lys	Ser	Phe	Gly	Arg	
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20	Ser	Ser	His	Leu	Ile	Gln	His	Gln	Thr	Ile	His	Thr	Gly	Glu	Lys	Pro	
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25	Ile	Gln	His	Gln	Arg	Thr	His	Ser	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Glu	
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	Glu	Cys	Gly	Lys	Ser	Phe	Ser	Arg	Ser	Ser	His	Leu	Ala	Gln	His	Gln	
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	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	His	Glu	Cys	Gly	Arg	
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35	Gly	Phe	Ser	Glu	Arg	Ser	Asp	Leu	Ile	Lys	His	Tyr	Arg	Val	His	Thr	
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	Gly	Glu	Arg	Pro	Tyr	Lys	Cys	Asp	Glu	Cys	Gly	Lys	Asn	Phe	Ser	Gln	
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				245						250					255		
	Tyr	His	Cys	Asn	Glu	Cys	Gly	Glu	Asn	Phe	Ser	Arg	Ile	Ser	His	Leu	
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	Val	Gln	His	Gln	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Thr	
			275					280					285				
50	Ala	Cys	Gly	Lys	Ser	Phe	Ser	Arg	Ser	Ser	His	Leu	Ile	Thr	His	Gln	
	290						295					300					
	Lys	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	Trp	Arg	
	305				310						315					320	
55	Ser	Phe	Gly	Glu	Arg	Ser	Asp	Leu	Ile	Lys	His	Gln	Arg	Thr	His	Thr	
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	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Val	Gln	Cys	Gly	Lys	Gly	Phe	Thr	Gln	
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5	Ser	Ser	Asn	Leu	Ile	Thr	His	Gln	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	
			355					360					365				
	Tyr	Glu	Cys	Thr	Glu	Cys	Asp	Lys	Ser	Phe	Ser	Arg	Ser	Ser	Ala	Leu	
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Leu Gln Gln His Gln Arg Thr His Thr Gly Glu Lys
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 <213> Human immunodeficiency virus
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 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
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 35 <223> Basic dimerization peptide
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<400> 23

Gly Gly Gly Gly Ser
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26

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<222> (15)..(15)
 <223> Amino acid 15 is "Xaa" wherein "Xaa" = is any amino acid.

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Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Asp Ser Xaa Ala

1 5 10 15

10

Leu Gln Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys
 20 25 30

Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser Ser Asn Leu Gln Lys His
 35 40 45

15

Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly
 50 55 60

20

Lys Ser Phe Ser Arg Ser Asp His Leu Gln Arg His Gln Arg Thr His
 65 70 75 80

Thr Gly Glu Lys

25

<210> 31
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 <223> Degenerate DNA probe

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<220>
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 <222> (7)..(10)
 <223> Nucleotides 7-10 are "n" wherein "n" = g, a, t, or c.

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<400> 31
 ggggaannnn

10

45

<210> 32
 <211> 26
 <212> DNA
 <213> Artificial Sequence

50

<220>
 <223> Zinc finger domain target sequence

55

<220>
 <221> misc_feature
 <222> (14)..(16)
 <223> Nucleotides 14-16 are "n" wherein "n" = g, a, t, or c.

<400> 32
 tatatatagg ggaannngta tatata

26

5	<210> 33 <211> 26 <212> DNA <213> Artificial Sequence	
10	<220> <223> Zinc finger domain target sequence	
15	<220> <221> misc_feature <222> (15)..(17) <223> Nucleotides 15-17 are "n" wherein "n" = g, a, t, or c.	
	<400> 33 tatatatagg ggaannnata tatata	26
20	<210> 34 <211> 26 <212> DNA <213> Artificial Sequence	
25	<220> <223> Zinc finger domain target sequence	
30	<220> <221> misc_feature <222> (15)..(17) <223> Nucleotides 15-17 are "n" wherein "n" = g, a, t, or c.	
35	<400> 34 tatatatagg ggaannntta tatata	26
40	<210> 35 <211> 26 <212> DNA <213> Artificial Sequence	
45	<220> <223> Zinc finger domain target sequence	
50	<220> <221> misc_feature <222> (15)..(17) <223> Nucleotides 15-17 are "n" wherein "n" = g, a, t, or c.	
55	<400> 35 tatatatagg ggaannncta tatata	26
	<210> 36 <211> 60 <212> DNA <213> Artificial Sequence	

<220>
 <223> Partial zinc finger domain oligomer

5 <220>
 <221> misc_feature
 <222> (45)..(56)
 <223> Nucleotides 45-47 and 51-56 are "n" wherein "n" = g, a, t, or c.

10 <400> 36
 ggggagaagc cgtataaatg tccggaatgt ggtaaaagtt ttagcnnnag cnnnnnnnttg 60

15 <210> 37
 <211> 60
 <212> DNA
 <213> Artificial Sequence

20 <220>
 <223> Partial zinc finger domain oligomer

25 <220>
 <221> misc_feature
 <222> (37)..(51)
 <223> Nucleotides 37-39 and 46-51 are "n" wherein "n" = g, a, t, or c.

30 <400> 37
 tttgtatggt ttttcaccgg tatgggtacg ctgatgnnnc tgcaannnnn ngctnnngct 60

35 <210> 38
 <211> 60
 <212> DNA
 <213> Artificial Sequence

40 <220>
 <223> Partial zinc finger domain oligomer

45 <220>
 <221> misc_feature
 <222> (46)..(57)
 <223> Nucleotides 46-48 and 52-57 are "n" wherein "n" = g, a, t, or c.

50 <400> 38
 ggtgaaaaac catacaaagc tccagagtgc ggcaaattct tctctnnntc tnnnnnnnctt 60

55 <210> 39
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Partial zinc finger domain oligomer

<220>
 <221> misc_feature

<222> (37)..(51)
<223> Nucleotides 37-39 and 46-51 are "n" wherein "n" = g, a, t, or c.

<400> 39

5 cttgtaaggc ttctcgccag tgtgagtagc ctgatgnnnc tgaagnnnnn nagannnaga 60

<210> 40

10 <211> 56

<212> DNA

<213> Artificial Sequence

<220>

15 <223> Partial zinc finger domain oligomer

<220>

<221> misc_feature

<222> (48)..(58)

20 <223> Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or c.

<400> 40

ggcgagaagc cttacaagtg ccctgaatgc gggaagagct ttagtnnnag tnnnnn 56

<210> 41

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Partial zinc finger domain oligomer

<220>

35 <221> misc_feature

<222> (28)..(48)

<223> Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" =
g, a, t, or c

<400> 41

40 cttctccccc gtgtgcgtgc gttggtgnnn ttgtaannnn nactnnnac taaag 55

<210> 42

45 <211> 45

<212> DNA

<213> Artificial Sequence

<220>

50 <223> PCR primer

<400> 42

gggcccggtc tcgaattcgg ggagaagccg tataaatgtc cggaa 45

<210> 43

55 <211> 48

	<212> DNA	
	<213> Artificial Sequence	
5	<220>	
	<223> PCR primer	
	<400> 43	
	cccggggggtc tcaagctttt acttctcccc cgtgtgcgtg cgttggtg	48
10		
	<210> 44	
	<211> 10	
	<212> DNA	
15	<213> Beet curly top virus	
	<400> 44	
	ttgggtgctc	10
20		
	<210> 45	
	<211> 60	
	<212> DNA	
25	<213> Artificial Sequence	
	<220>	
	<223> Partial zinc finger domain oligomer	
	<400> 45	
30	ggggagaagc cgtataaatg tccggaatgt ggtaaaagtt ttagcaccag cagcgatttg	60
	<210> 46	
	<211> 60	
35	<212> DNA	
	<213> Artificial Sequence	
	<220>	
40	<223> Partial zinc finger domain oligomer	
	<400> 46	
	tttgtatggt ttttcaccgg tatgggtacg ctgatgacgc tgcaaatacg tgctggtgct	60
45		
	<210> 47	
	<211> 60	
	<212> DNA	
	<213> Artificial Sequence	
50	<220>	
	<223> Partial zinc finger domain oligomer	
	<400> 47	
55	ggtgaaaaac catacaaatg tccagagtgc ggcaaattct tctctacctc tgatcatctt	60
	<210> 48	

	<211> 60	
	<212> DNA	
	<213> Artificial Sequence	
5	<220>	
	<223> Partial zinc finger domain oligomer	
	<400> 48	
10	cttgtaaggc ttctcgccag tgtgagtacg ctgatgacgc tgaagatgat cagaggtaga	60
	<210> 49	
15	<211> 56	
	<212> DNA	
	<213> Artificial Sequence	
	<220>	
20	<223> Partial zinc finger domain oligomer	
	<400> 49	
	ggcgagaagc cttacaagtg ccctgaatgc gggaagagct ttagtcgtag tgatag	56
25	<210> 50	
	<211> 55	
	<212> DNA	
	<213> Artificial Sequence	
30	<220>	
	<223> Partial zinc finger domain oligomer	
	<400> 50	
35	cttctccccc gtgtgcgtgc gttggtgggt ttgtaagcta tcactacgac taaag	55
	<210> 51	
40	<211> 16	
	<212> DNA	
	<213> Arabidopsis	
	<400> 51	
	atagtttacg tggcat	16
45	<210> 52	
	<211> 10	
	<212> DNA	
50	<213> Arabidopsis	
	<400> 52	
	atagtttacg	10
55	<210> 53	
	<211> 10	
	<212> DNA	

	<213> Arabidopsis	
5	<400> 53 tacgtggcat	10
10	<210> 54 <211> 45 <212> DNA <213> Artificial Sequence	
15	<220> <223> PCR primer	
	<400> 54 ttcagggcgg tctctcggct tctcgccagt gtgagtacgc tgatg	45
20	<210> 55 <211> 44 <212> DNA <213> Artificial Sequence	
25	<220> <223> PCR primer	
30	<400> 55 cgaattcggg tctcagccgt ataaatgtcc ggaatgtggt aaaa	44
35	<210> 56 <211> 45 <212> DNA <213> Artificial Sequence	
40	<220> <223> PCR primer	
	<400> 56 tgcggccggg tctctcggct tctccccctg gtgcgtgcgt tgggtg	45
45	<210> 57 <211> 19 <212> DNA <213> Artificial Sequence	
50	<220> <223> ZFP target sequence	
	<400> 57 ttgggtgctt tgggtgctc	19
55	<210> 58 <211> 10 <212> DNA	

	<213> Artificial Sequence	
	<220>	
5	<223> ZFP target sequence	
	<400> 58	
	ttgggtgctt	10
10	<210> 59	
	<211> 10	
	<212> DNA	
	<213> Artificial Sequence	
15	<220>	
	<223> ZFP target sequence	
	<400> 59	
20	ttgggtgctc	10
	<210> 60	
	<211> 35	
25	<212> DNA	
	<213> Artificial Sequence	
	<220>	
	<223> ZFP target probe	
30	<400> 60	
	tatatatatt ggggtgctttg ggtgctctat atata	35
35	<210> 61	
	<211> 10	
	<212> DNA	
	<213> Artificial Sequence	
40	<220>	
	<223> ZFP target sequence	
	<400> 61	
45	agtaaggtag	10
	<210> 62	
	<211> 10	
	<212> DNA	
50	<213> Artificial Sequence	
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	<223> ZFP target sequence	
55	<400> 62	
	ttgggtgctc	10

	<210> 63	
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5	<212> DNA	
	<213> Artificial Sequence	
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10	<400> 63	
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15	<210> 64	
	<211> 10	
	<212> DNA	
	<213> Artificial Sequence	
	<220>	
20	<223> ZFP target sequence	
	<400> 64	
	ggagatgata	10
25	<210> 65	
	<211> 19	
	<212> DNA	
	<213> Artificial Sequence	
30	<220>	
	<223> ZFP target sequence	
35	<400> 65	
	ttgggtgctt tgggtgctc	19
40	<210> 66	
	<211> 19	
	<212> DNA	
	<213> Artificial Sequence	
	<220>	
45	<223> ZFP target sequence	
	<400> 66	
	agtaaggtag gagatgata	19
50	<210> 67	
	<211> 19	
	<212> DNA	
	<213> Artificial Sequence	
55	<220>	
	<223> ZFP target sequence	

<400> 67
tacgtggcat tgggtgctc

19

5 <210> 68
<211> 28
<212> PRT
<213> Artificial Sequence

10 <220>
<223> Zinc finger domain

15 <220>
<221> VARIANT
<222> (13)..(13)
<223> Amino acid 13 is "Xaa" wherein "Xaa" = Z1 wherein Z1 = Arg, Gln,
Thr, Met or Glu

20 <220>
<221> VARIANT
<222> (15)..(15)
<223> Amino acid 15 is "Xaa" wherein "Xaa" = Z2 wherein Z2 = Ser, Asn,
Thr, or Asp

25 <220>
<221> VARIANT
<222> (16)..(16)
<223> Amino acid 16 is "Xaa" wherein "Xaa" = Z3 wherein Z3 = His, Asn,
Ser, or Asp

30 <220>
<221> VARIANT
<222> (19)..(19)
<223> Amino acid 19 is "Xaa" wherein "Xaa" = Z6 wherein Z6 = Arg, Gln,
Thr, Tyr, Leu, or Glu

35 <400> 68

40 Gln His Ala Cys Pro Glu Cys Gly Lys Ser Phe Ser Xaa Ser Xaa Xaa
1 5 10 15

Leu Gln Xaa His Gln Arg Thr His Thr Gly Glu Lys
20 25

45 <210> 69
<211> 28
<212> PRT
<213> Artificial Sequence

50 <220>
<223> Zinc finger domain

55 <220>
<221> VARIANT
<222> (13)..(13)
<223> Amino acid 13 is "Xaa" wherein "Xaa" = Z1 wherein Z1 = Arg, Gln,
Thr, Met, or Glu

<220>
 <221> VARIANT
 <222> (15)..(15)
 <223> Amino acid 15 is "Xaa" wherein "Xaa" = Z2 wherein Z2 = Ser, Asn,
 Thr, or Asp.

5

<220>
 <221> VARIANT
 <222> (16)..(16)
 <223> Amino acid 16 is "Xaa" wherein "Xaa" = Z3 wherein Z3 = His, Asn,
 Ser, or Asp

10

<220>
 <221> VARIANT
 <222> (19)..(19)
 <223> Amino acid 19 is "Xaa" wherein "Xaa" = Z6 wherein Z6 = Arg, Gln,
 Thr, Tyr, Leu, or Glu.

15

<400> 69

20

Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Xaa Ser Xaa Xaa
 1 5 10 15

25

Leu Ser Xaa His Gln Arg Thr His Thr Gly Glu Lys
 20 25